



SEQ.ST25
SEQUENCE LISTING

11

<110> Gonzalgo, Mark L.

Jones, Peter A.

Liang, Gangning

<120> CANCER DIAGNOSTIC METHOD BASED UPON DNA METHYLATION DIFFERENCES

<130> 47675-21

<140> 09/887,941

<141> 2001-06-22

<150> US 09/094,207

<151> 1998-06-09

<160> 17

<170> PatentIn version 3.1

<210> 1

<211> 530

<212> DNA

<213> homo sapiens

<400> 1
cccgcgacct aagccagcga cttaccacgt tagtcagcta agaagtggca gagctgggat 60
tcgaacctat aaagaactct gaagcctggg tatttttaca tgacacttta cataatgcgc 120
cacggggtag tcggaggggg aggtccatct ccctttccct tgctgtccat ctccacagaa 180
aagaagcaag tggaggacag gagccagaaa gtcactctggc cgcggatcat tccggagtga 240

SEQ.ST25

ccccgcgcgc caccactcgc atagtcgcgt tatggcgga gggcacctca gagattctca	300
caggggctgt gcggccagaa ccagaagtgc aaagcaccgt tagcgactct atcgcccct	360
gccgcctgtg gcgcccagtc cgaagctgct gttttcagga gggctagtgg gctaagaaaa	420
gagctcaccg actgactgcc caacagctgt tgcgagccag tgctaggctg cagacagcct	480
tgccaaatgt ggtgacataa gcgggagggg ggaacattta gagagcccta	530

<210> 2

<211> 308

<212> DNA

<213> homo sapiens

<400> 2

ctagggtagg ctggtctgtg ctggatacgc gtgttcttct gcggagttaa agggtcgggg	60
acgggggttc tggacttacc agagcaattc cagccggtgg gcgtttgaca gccacttaag	120
gaggtaggga aagcgagctt caccgggcgg gctacgatga gtagcatgac gggcagcagc	180
agcagcagcc agcaaaagcc tagcaaagtg tccagctgct gcaactgccgc ggggactccc	240
acatcaccat gactagtgtg gcaactctgc agcagaaacg gcttccgagg aacacaggat	300
cgcggggg	308

<210> 3

<211> 177

<212> DNA

<213> homo sapiens

<400> 3

gcttcctttt tctcggttt cctcactatc ctctccctgt tcgagagtat ctccaccagc	60
accgagcctc acacgggctg tgcctccatc tttggaatgc ctacccttct ttcttgcgaa	120
gcccctccca gggccagccc ttgtgcaccg gctcaagggg actgctctcc tgccctcg	177

<210> 4

<211> 148

<212> DNA

SEQ.ST25

<213> homo sapiens

<400> 4

ttgcgccgat cgtcaagaac ctctcatccc tggcagcagc aaagccaata tatttccatt 60

tcttatttca gtttgccacc aaaacaaagc tgcgcgcggc tgagggcagg aaggcgctga 120

gaccgaccga gaagaaggga cgtcccgg 148

<210> 5

<211> 384

<212> DNA

<213> homo sapiens

<400> 5

caggcccgcc gagactccac tccaactacc aggaaatttc ccgtggagct tcaattcctg 60

ggaccctcct actgcgggga gagtggtttc cctgccccac accatgccct aggcccagat 120

ctgcggctct tgggggatct ctccgagctc cgacaccgtg ttcggaccgg gtgcgccttg 180

ccgctggggc tcaagcctgc aggcgtgaga accgggggac tctctatggc accaagagct 240

tcaccgtgag cgtaggcaga agcttcgctt tgatcctagg gcttacaag tcctcctttg 300

gctgcccattg atggtaaaag ggcagttgct cacaagcgc gagtgtgtgt gccagacagt 360

gtaaatgagt gttgggaccg gcgt 384

<210> 6

<211> 178

<212> DNA

<213> homo sapiens

<400> 6

gggtccgttc gtgaatgcat gaggagggtg tgagcgccag ggggttacac ttctcacggg 60

ttaaaacca gacaattca cgagggaacc acgtgccatt ttaacagcgt acggtcggga 120

tcgtgggacg tcattaaacg gagtggggtg agtatgtgac tctgtcacc attttctg 178

<210> 7

<211> 359

SEQ.ST25

<212> DNA

<213> homo sapiens

<400> 7

ccccgcgggg	cagaatccaa	gtgagtcaga	cacattgctc	cctccctgct	gctgccagtc	60
catctctttg	ccaacaaacc	tgcttaaaat	gccaaagctg	gtccaaagtt	tcaggaaaac	120
aacttccgcc	agagggcacg	tagagggcac	agatgctata	gatgcttctc	tgacaaacac	180
tcctgacccc	cttgacagat	tggaaaatac	atggttcaga	aagggtgaga	gatttcaact	240
tgagaagtga	aactaggaaa	agatggaagg	tgtccggatt	tctagctcaa	gtccacacac	300
tgcttctgct	gcggtgacta	aatcgtggct	gtgttctcat	cacctgcctc	gcggcgcg	359

<210> 8

<211> 251

<212> DNA

<213> homo sapiens

<400> 8

ggcgggcctg	ggcaccgcgg	agggggggct	tttctgcgcc	cggcgaagcg	tggaacttgc	60
gccctgaggg	agcgcggcga	gaccagtcca	gagaccgggg	cgagcctcct	caggattcct	120
cgccccagtg	cagatgctgt	gagcttagac	gaggacaggg	catggcactc	ggcttggccc	180
gtagtggacg	gtgtttttgc	agtcatgaac	ccaaacgccg	caaaccttga	ccgtttcccc	240
accctgtttg	t					251

<210> 9

<211> 145

<212> DNA

<213> homo sapiens

<220>

<221> misc_feature

<222> (126)..(126)

SEQ.ST25

<223> a, g, c or t sequence variation may exist at this position

<220>

<221> misc_feature

<222> (127)..(127)

<223> a, g, c or t sequence variation may exist at this position

<400> 9
 tgagagcagc atcctcccct gcgtgtggtt ctctaactta cctcctgtat ggggtctgcg 60
 gaccagcac acctcccgga cccccaaaa attccagctc aagagcccta aaaatcctta 120
 ccctgnnaaa gtttgagctt ctccc 145

<210> 10

<211> 215

<212> DNA

<213> homo sapiens

<400> 10
 acgccggcca cagttcttca gtgaaacgct tcaactctctg gtcataagagg taggaaacta 60
 tagctgtccc aactaaatgt caggacgaat tagcccagct ggtcacgctc acagtcaccg 120
 cctccaccag actgagcgac cctcccaacg gggtttgccg tggtgggagg acagcggagt 180
 ttcgttgctg tgtcaatttg tgtagacgcg gctgc 215

<210> 11

<211> 220

<212> DNA

<213> homo sapiens

<400> 11
 ctgctctctt ctcttctttt cccctttcct ctctctctcc tttctcagg tcacagcgga 60
 gtgaatcagc tcggtggtgt ctttgtcaac gggcggccac tgccggactc caccggcag 120
 aagattgtag agctagctca cagcggggcc cggccgtgcg acatttcccg aattctgcag 180

SEQ.ST25

gtgatcctcc cggcgccgcc ccaactcgccg cccccgcggc 220

<210> 12

<211> 196

<212> DNA

<213> homo sapiens

<400> 12

gggcggcacg gagggagtca ggagtgagcc cgaagatgga gagaagtcga ttcgcccaga 60

gaacgcaaga cggcggatca gagatgagtc ccaggaacct cagagagcga ggctgacagg 120

cccggggaga ggaccgggca gggacaaacc agcggacaga gcagagcgcg aaatggttga 180

gaccgggaag cgacct 196

<210> 13

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> p16 promoter region-specific Ms-SNuPE primer

<400> 13

gtaggtgggg aggagtttag tt 22

<210> 14

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> p16 promoter region-specific Ms-SNuPE primer

<400> 14

tctaataacc aaccaacccc tcc 23

SEQ.ST25

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> p16 promoter region-specific Ms-SNuPE primer

<400> 15

tttttttggt tggaagata t

21

<210> 16

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> p16 promoter region-specific Ms-SNuPE primer

<400> 16

ttttaggggt gttatatt

18

<210> 17

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> p16 promoter region-specific Ms-SNuPE primer

<400> 17

tttgagggat aggggt

15